

1/28

AIM-1 OLIGONUCLEOTIDES

-Oligonucleotide primers used during Long Distance Inverse PCR
-Oligo's bind to regions of AIM-1 (Mungbean ACC Synthase).

NSE-1

5'-GCGGAT[↓]CCATCTTGGACAACAAGGGAGTT- 3' 4
29'omer
Tm = 68

NSE-2

5'-TAGGATC[↓]CAGAAAGACACTGAGAACCGTGG- 3' 5
30'omer
Tm = 70

NSE-3

5'-ACGGATCC[↓]GGTGTATGTGGTTAGAGTGTG- 3' 6
29'omer
Tm = 62

NSE-4

5'-CAGGATC[↓]CAGACATAGAGTGTGACCGCAA- 3' 7
29'omer
Tm = 66

NSE-5

5'-ATCGATCATATGAGCTCTAGACCCGGGCTGCAGGATCC[↓]GGTGTATGTGGTTAGAGTGTG- 3' 8
59'omer
Tm = 62

note: NSE-5 is identical to NSE-3 except different restriction enzyme sites have been incorporated
(ie. 5'-Cla I, Nde I, Sac I, Xba I, Sma I, Pst I & Bam HI-3')

NSE-6

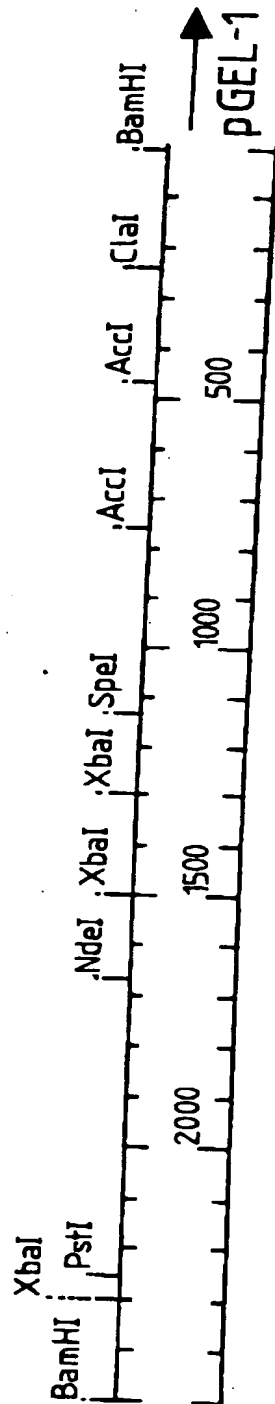
5'-CCGCGGAGATCTATCGATCTCGAGAATTCAAGCTT[↓]CAGACATAGAGTGTGACCGCAA-3' 9
57'omer
Tm = 66

note: NSE-6 is identical to NSE-4 except different restriction enzyme sites have been incorporated
(ie. 5'-Sac II, Bgl II, Cla I, Xho I, Eco RI, & Hind III-3')

FIGURE 1

Substitute Sheet
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2/28



(2,483bp)

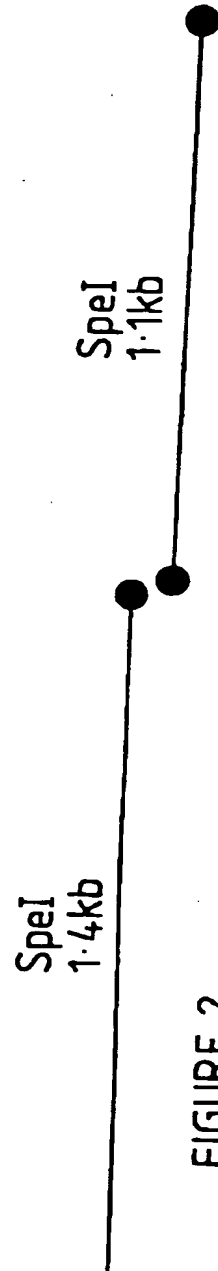
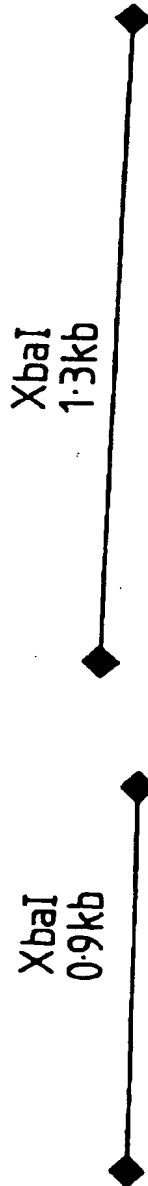
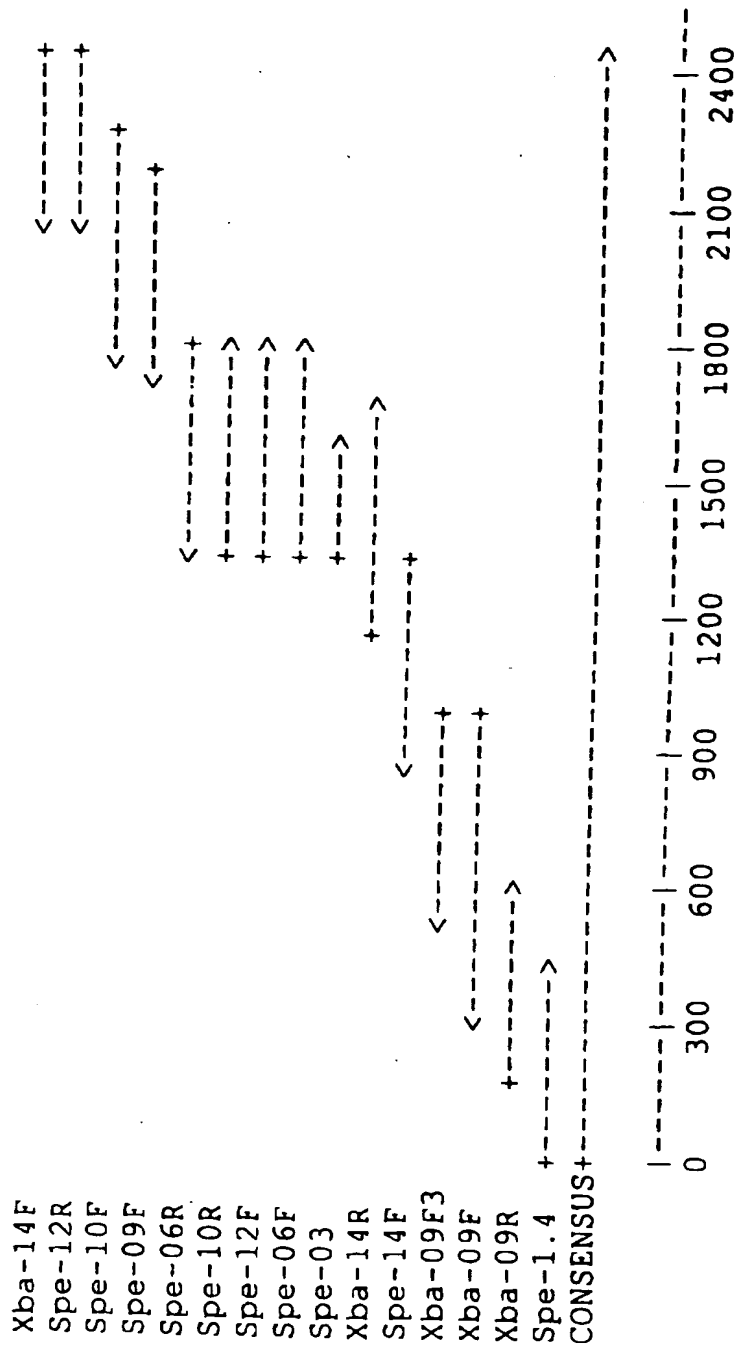
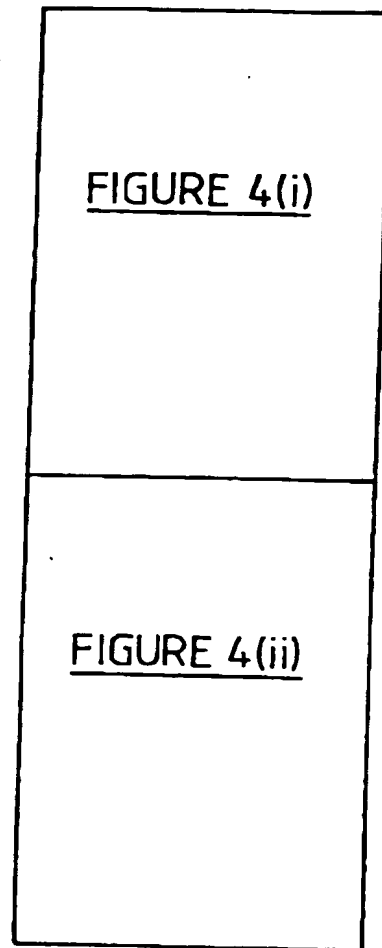


FIGURE 2

3/28

pGEL-1 2.5Kb promoter sequencing strategy:**All fragments****FIGURE 3**

4/28

FIGURE 4

pGEL-1 2.5Kb Promoter Fragment 5/28

Length: 2470

1 TTACAGATAC ACAGAATCAG ACGACACATC TACTTTAATA ACAGAAAAAT
51 AATAAGTGTC GGAGATTATG GTACGACAAG ATGAAATGTT TTTATATGGT
101 TGAGATTATT TTGGTCTGTT GTTGGAAGTT TCACGAATCA TGATTTTGAT
151 TTTACGTATT AAAAAATGAA AAGTTGAATC ATGCATTTTA TCTAGAAGCT
201 GGGAACTGAA CCAAAAAAAT AGCCAGTTGA ACAACTGCAG TATTTGTAGG
251 CGTATTCATT TCTCCTTTCC TACAATAATC CTTGGTTGCT CTTTATCGGA
301 AAAAAACCAA AAGCAATAGC TACTCTGTAA GGTCCCTCGAT TGCCGACAAG
351 AACATCACAT GCGTGCTGTC GAAGAACACA TAATTTTGAG GTTGAAGCTC
401 ACGTGCGAGT TTTGCATATT TTAGGTTAT GTGTACACGT ATGGAGTGAG
451 TTCCGCGTAT ATAGTGTAGG TAGTTGAGTG GCTGAGTAGC GAGTGAATCA
501 GGTAACACTA TCTTTTCAAG CCACCTAATT AAGGGATTTA ATGTTTCATGC
551 AACTGTTCTT CGCTAACTAA GGCCCCACTT ACCTTTATAA TATTCTCTCT
601 AACTCCGGGC TTTTGGTAAG TACAACCTTT CTACTCTTAT TTAATGGAGG
651 GATTATTTTT TCCATATACC AATTAATTTA TTTTFTAATT TATGCATTTT
701 GATCTTATAT TAAAACAATT ATGGTATGGA TTAAGTCGTA TATCGGTGAC
751 AATTGAAGTT TTCCTCAAGT TTAGCCATTT TTATGAAATT AAACCTTAATC
801 ACTACTATTA GGTAAATTCA TATGTATCAT TAACAATTTT AATGTGAGTT
851 CAATTTTACC CAAGATTGTA AAGTTGTTGT CAACTTCTGT TAACTAAAGT
901 TGTATTATAA GGTTGACGAC TTTAACCTAA ATCTATTTTG AATTGAAGGG
951 GTTGATGACT TCAGCTTTAA AATAATTCAA CTAAAGTTCT AGACTACATT
1001 GGAGATTTTA GTGTCATAA AATTTTAGAA AAAGGCTGAG TTAAAGTTAT
1051 GAAAAAGATT GGTGACTATT CAATTAATTA GTTGTGAATT GATGACAAAT
1101 ATTTTCATGAG CATAACCAAT CAGAGAAATA CCACCTCGAC CGACTACAAC
1151 AATCTCAATG TTAATTAATG AAGCATTGTA GTATAAGGAG TCTAGAATAA
1201 ATTTCTTAAA TATTAGAGGA AACTATTTT TAAAAAATTA CAAGAAAAGT
1251 TTGATCTATA ACCTCTTTAA ACTTTAAATT ATCTAACAAT TTTCTTATGA

FIGURE 4(i)Substitute Sheet
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6/28

1301 CTCACATTGT GTTGATAGGG TGATTTTGTC AAAATATATG TCTATTTTAT
1351 ACTAGTATGA TTTGTCTGCG AATTATATAT AGTATTAAC TGGAGAAATG
1401 ATTGCCTAAT AAGTTATAAA AAAGGAGAAA ATATTTATTC ATAAAAAAA
1451 TACACTTAAA TAAGTAACAA TAATAAAAAA CATTATATAA GAGATTAAGA
1501 TAATTTAATA AGTATTGAAT GTAGAATAAT TTTTATTTAT AAATTTGAAC
1551 TAAAATATTC AAATAATATT CAAAGTAAAT AATAGATATA ATTCATCATT
1601 CAATACGAGT AATTCAATCT ATTATAATCC ATATATTAGA TAAATATACA
1651 AATATTTGTT AAATTTTACA TTATTATATT ACTAAATATA TATTAATTTT
1701 CTTTGAATAT CTTTTATACA AGTAGGTAGA CTAGAAGAAT TATCTTATCT
1751 CCCGTATATT TGTAGATGTT AAATGTAACG GGCTTAGACT GATGTTTTTG
1801 TATTATATTA TTTATAAATC CATTAGAGAT TTAAGTTAAT GTCTCTCTTT
1851 GATTTTAAAC ATGGTCTAAA AATTAGGTTT AATCATTGCG TCCTCAATGA
1901 ACCCATGCTA TATGTTTTAA AGTTTTTTGT TTTTGGACAA TGTTTTTTAT
1951 TTCTGAGATT GCTCTTAGGA TTGAAATTAT GTTTGATACT AGAAAACGAA
2001 GAAGTAGAGA GTAGTGTATA CACGTGTAAA AAATAATAGT TGTGGGAACT
2051 TAAGTTGGAT TTGAATACTA GGACGAGGCT GGAAGGGTTT CCACTAAGTT
2101 GACAAAAATT ATTACAAGTG GCAACTAGCT AGGTCTCACA AAGTATTACT
2151 AATTAATAGT GGGTCTGTCT GCATACCAAC TCTTGCCTAA TTTTCAAACA
2201 CCGCATTCTC TCTTCTTCTC TCCTTCTTCC TCTGGAAACT TCATCGATGT
2251 GGAATTCTGT CTCTCAAAAG TCAAGCTCAA TTTATCCAAT GCATTATAAA
2301 TACACACTCT CCCTCCCTTC TATTCTTCAT TGCATCACAT TTCCTCTATA
2351 AATTACTCAC ACCTTATTCC TAACTTCATT TCAACATCCT CTCTCCCACT
2401 TACTTCGATT TCATCAATTC CAATAAACTC AACACACTTT TTTACACTCC
2451 ACACTCTAAC CACATACACC

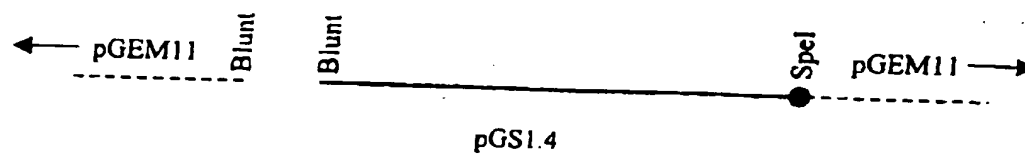
FIGURE 4(ii)

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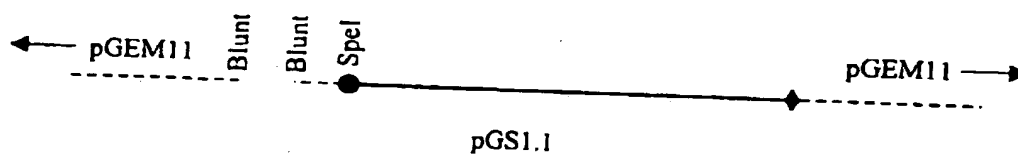
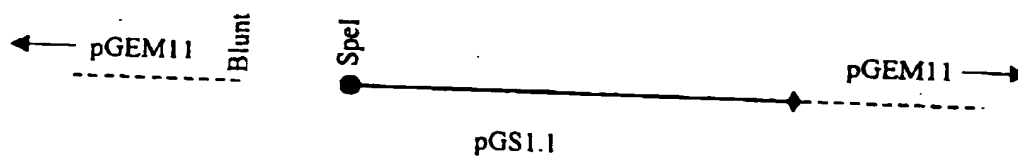
7/28

Reconstruction of 2.5 kb **pGEL-1** promoter

(a)

1. Cut *Hind*III and blunt end pGS1.42. Cut *Spe*I

(b)

1. Cut *Sall* and blunt end pGS1.12. Digest with *Spe*I

(c) Ligate (a) into (b)

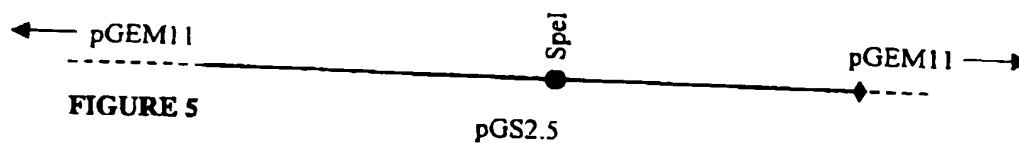
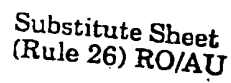


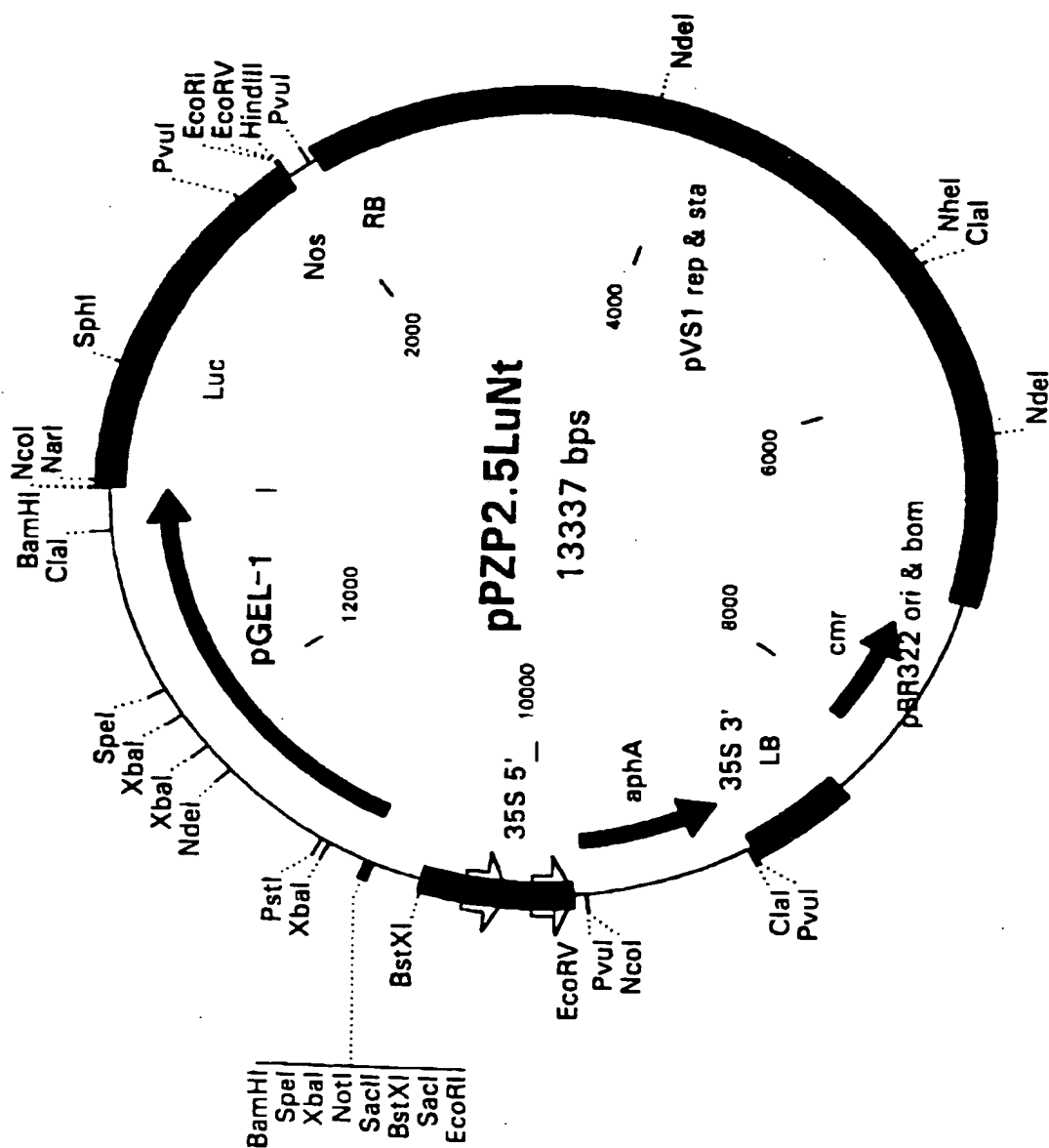
FIGURE 5

FIGURE 6A(i)



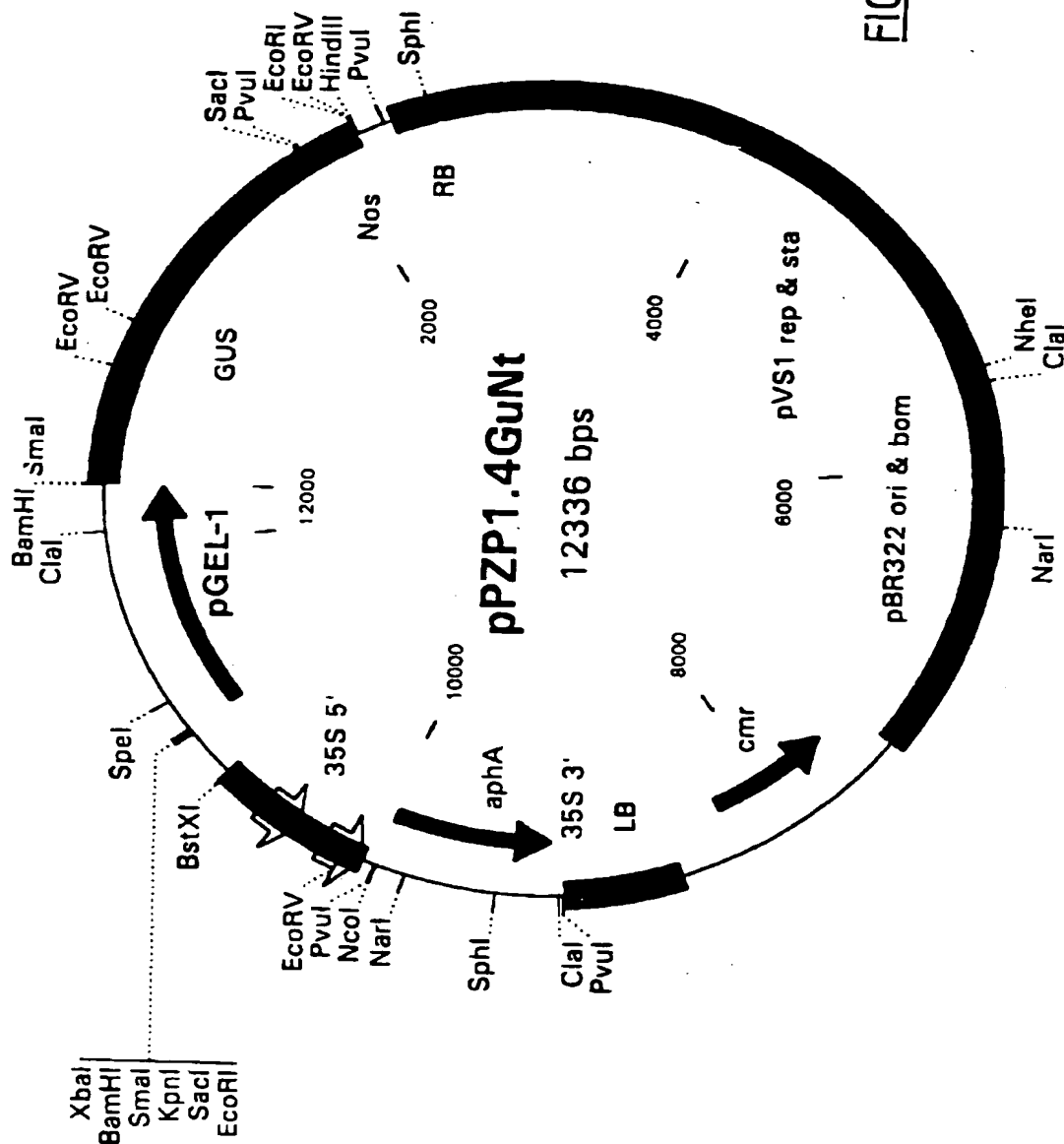
9/28

FIGURE 6A(ii)

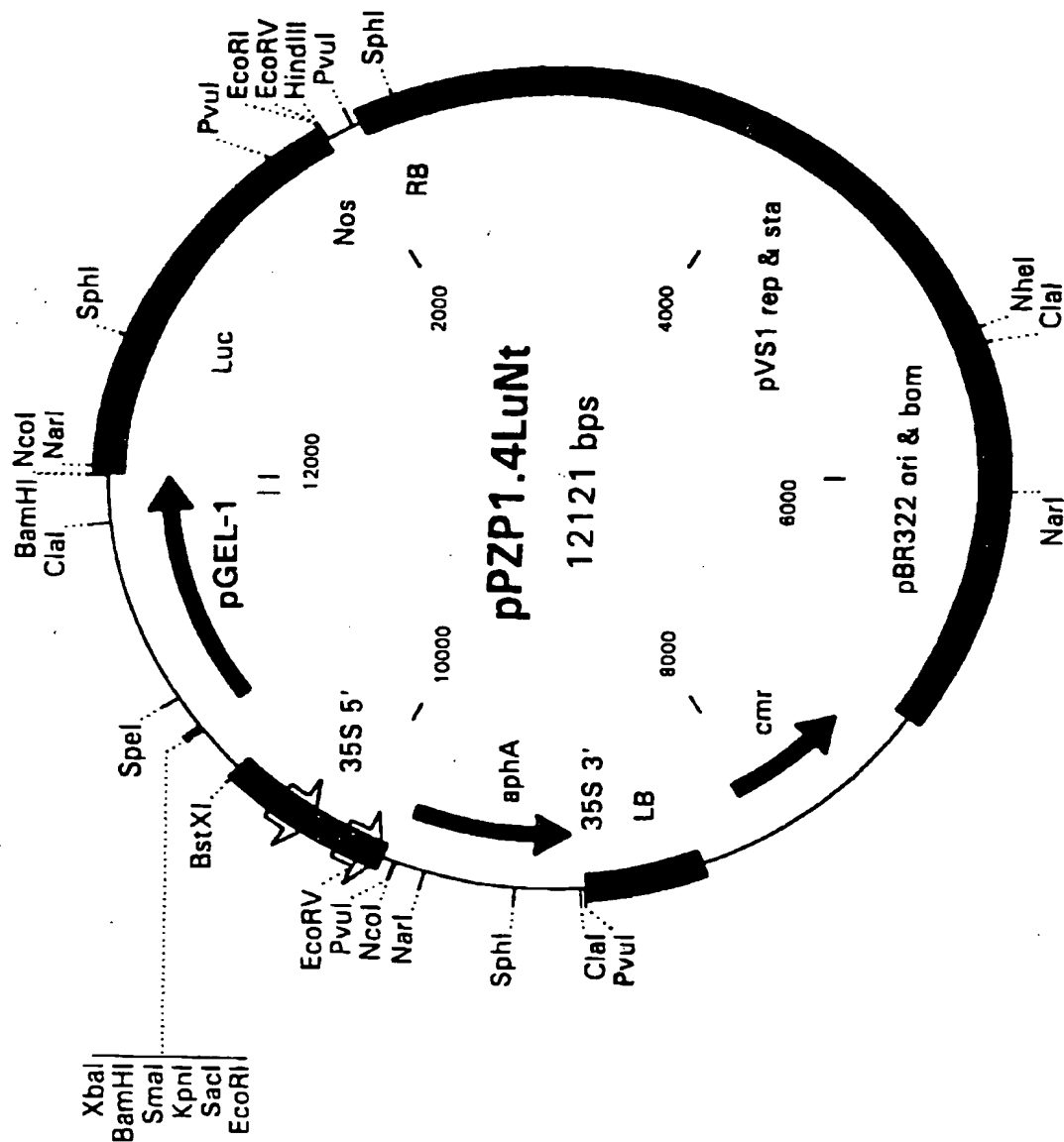


10/28

FIGURE 6A(iii)

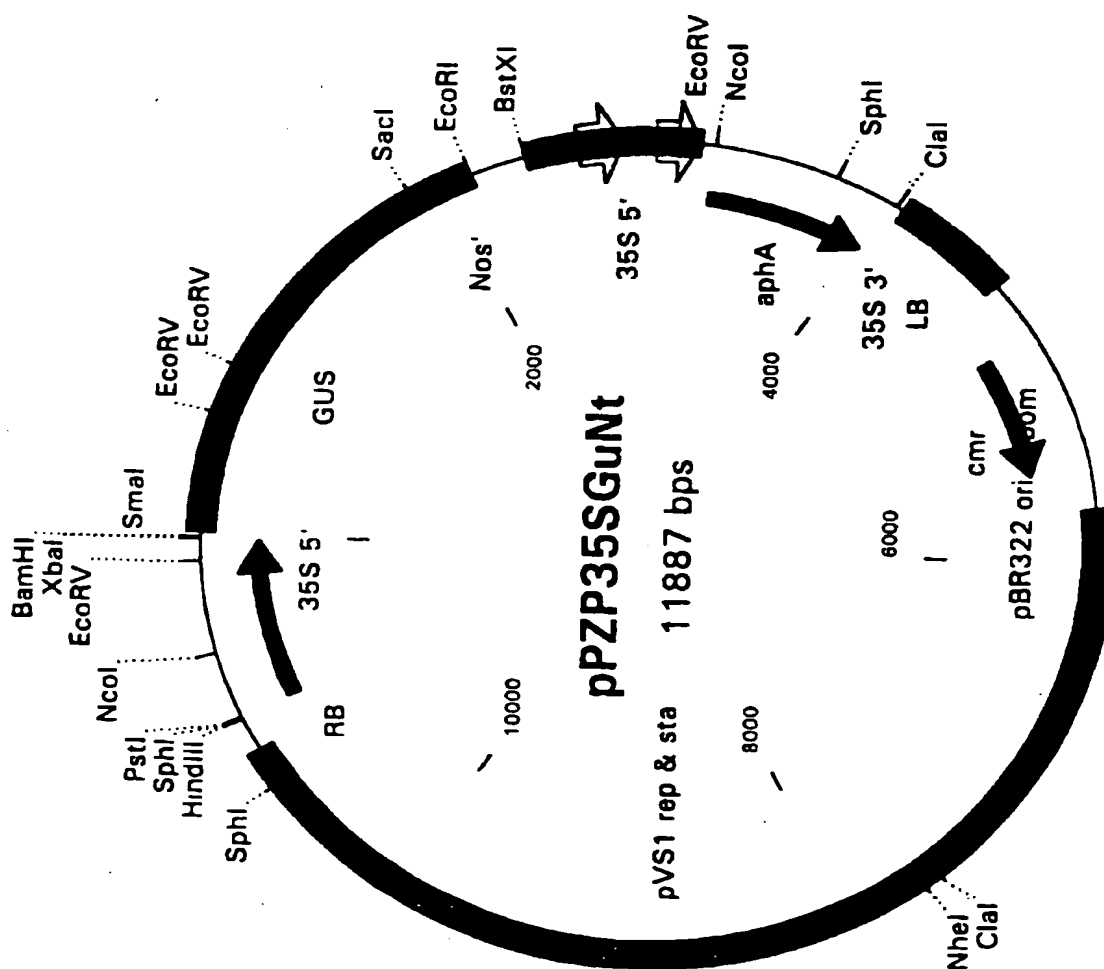


11/28

FIGURE 6A(iv)

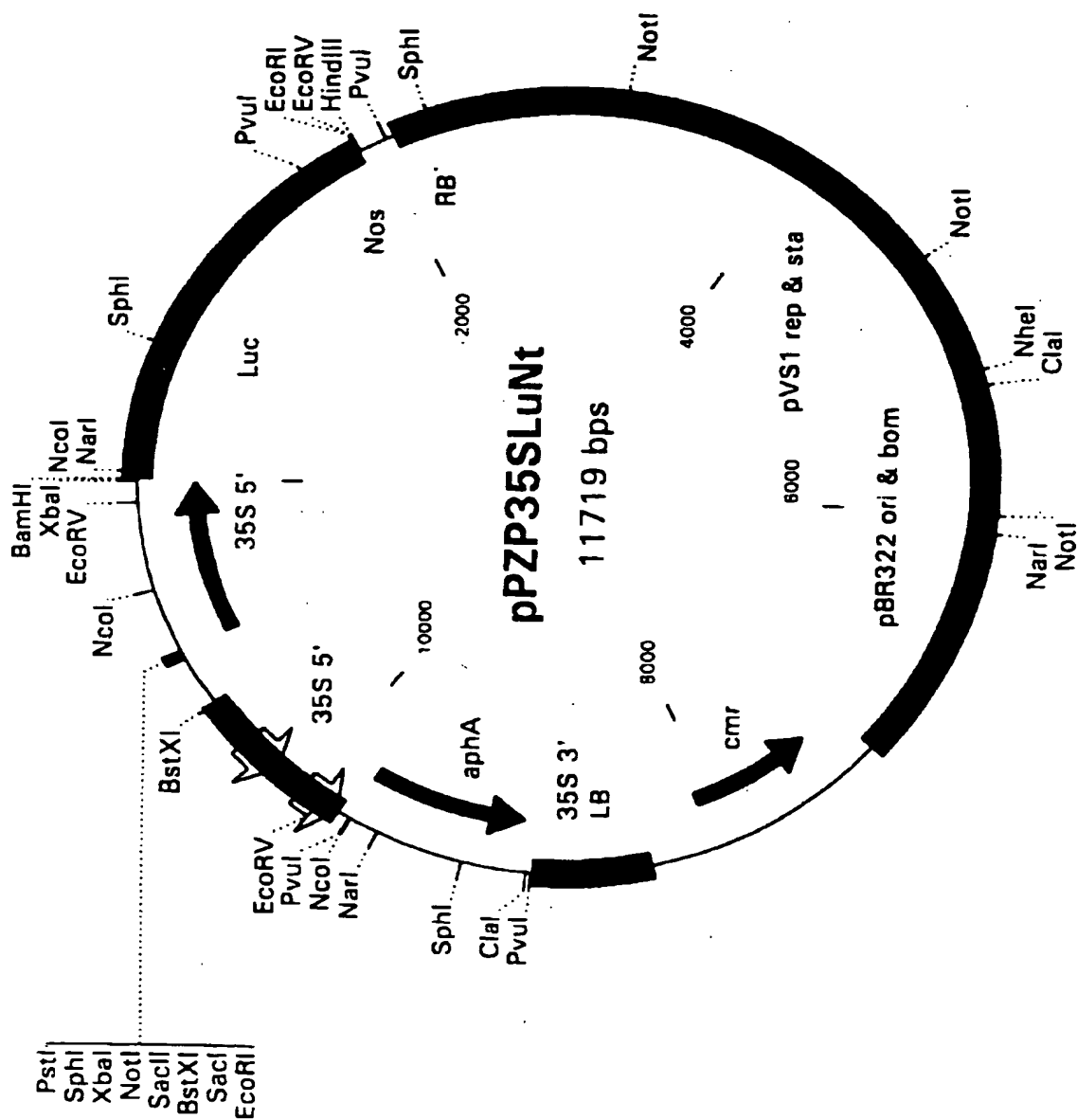
12 / 28

FIGURE 6A(v)



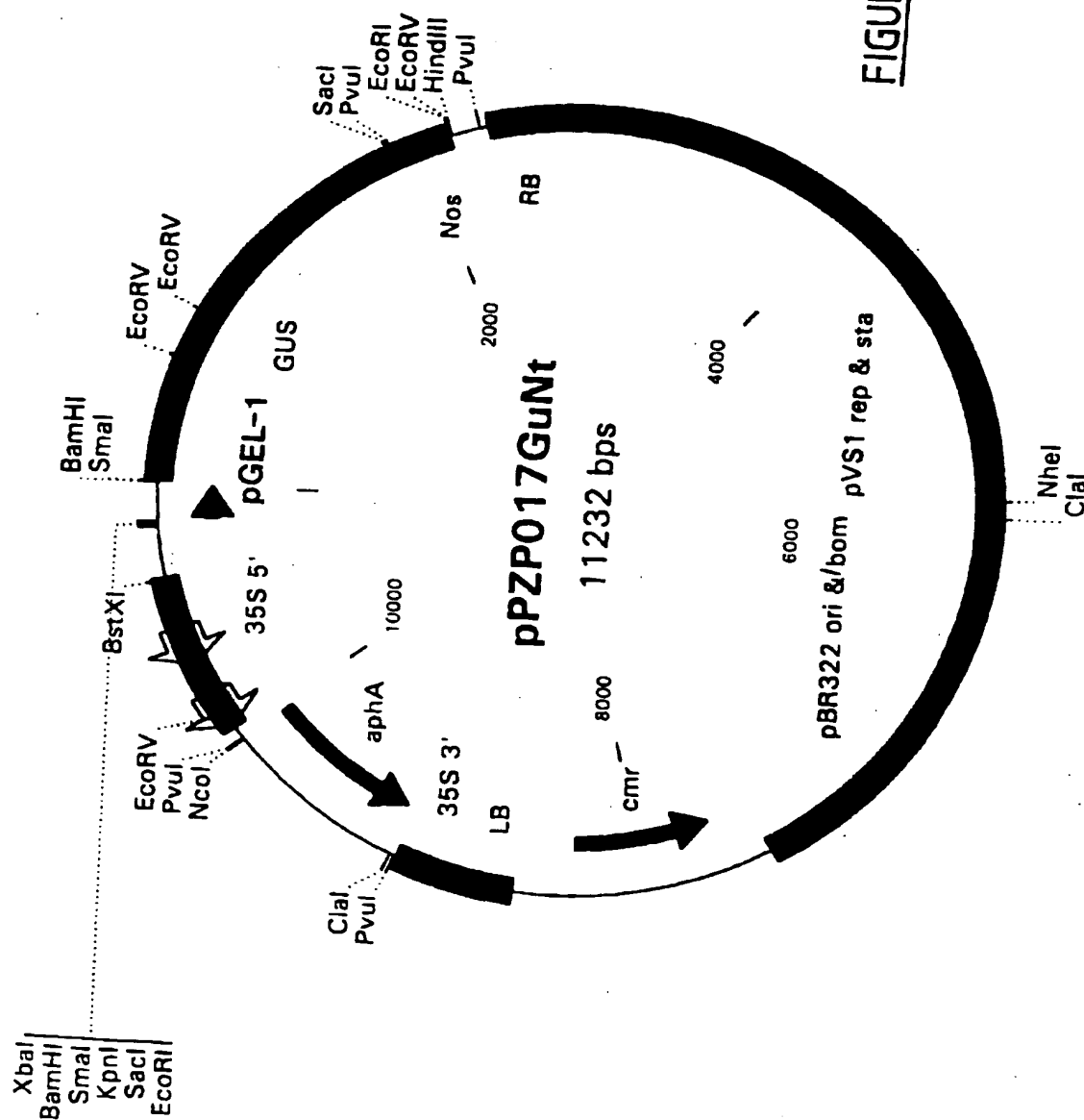
13/28

FIGURE 6A(vi)

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14/28

FIGURE 6A (vii)



Substitute Sheet
(Rule 26) RO/AU

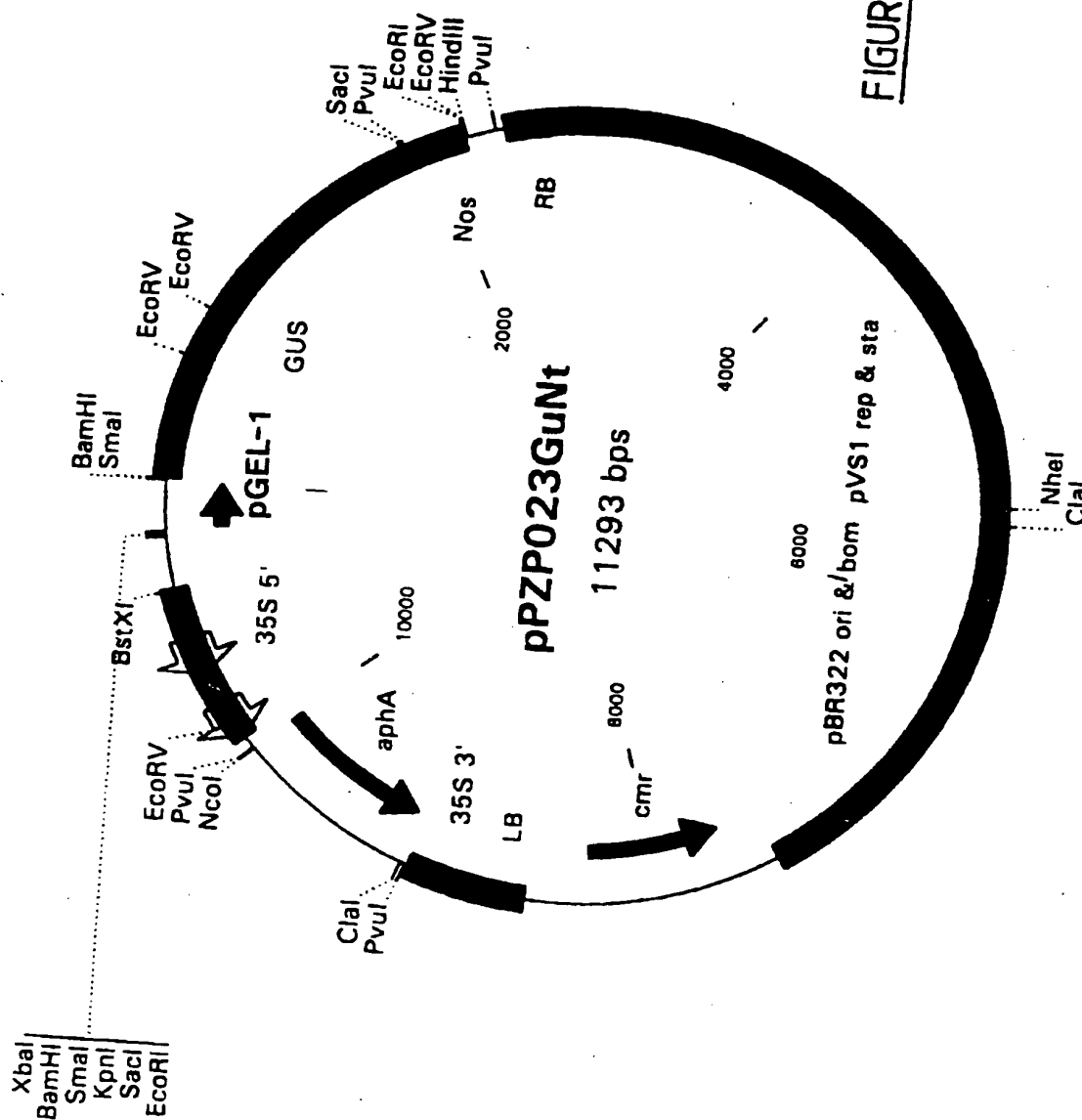
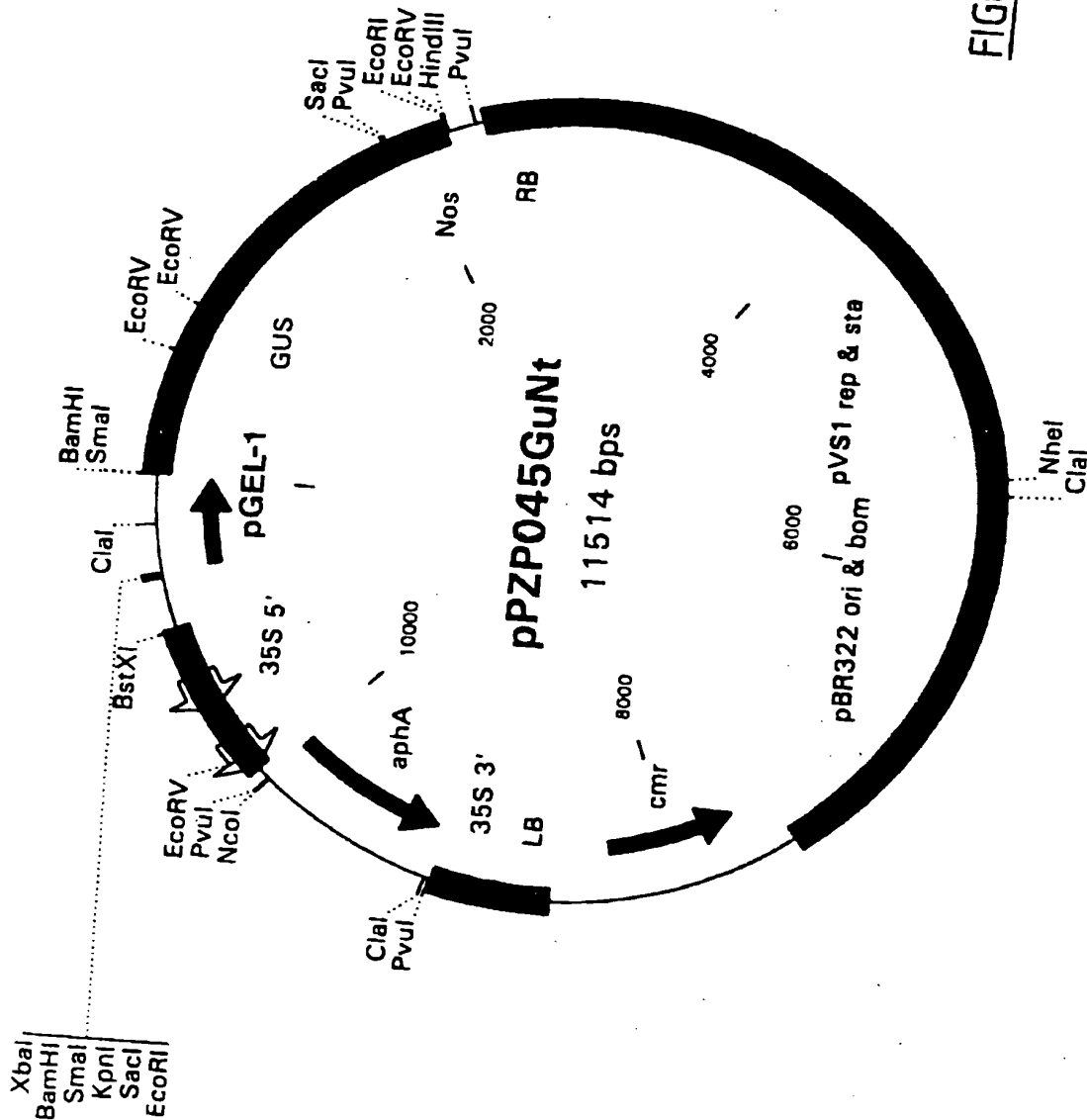
FIGURE 6A(viii)

FIGURE 6A(ix)



17 / 28

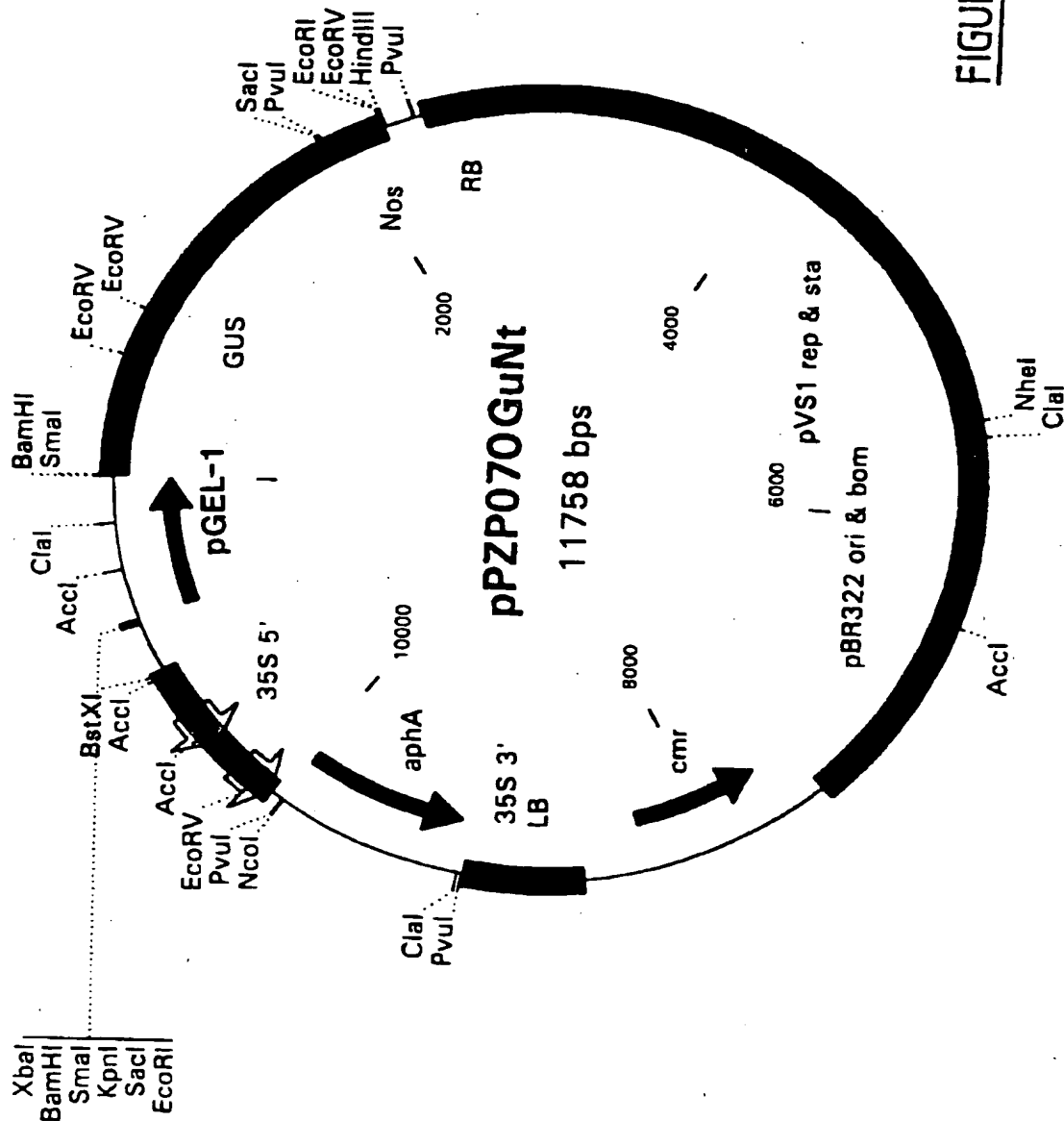


FIGURE 6A(x)

18/28

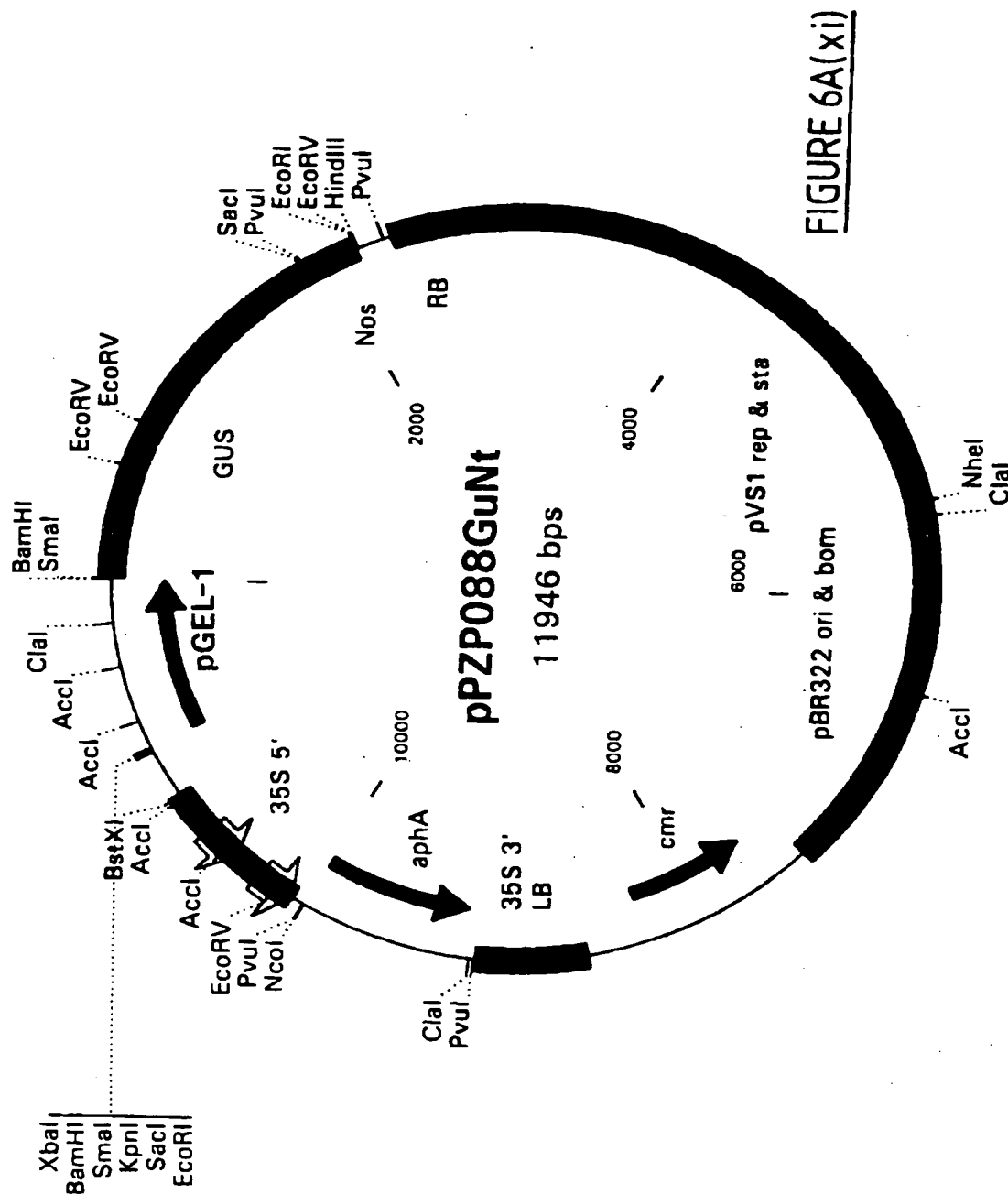
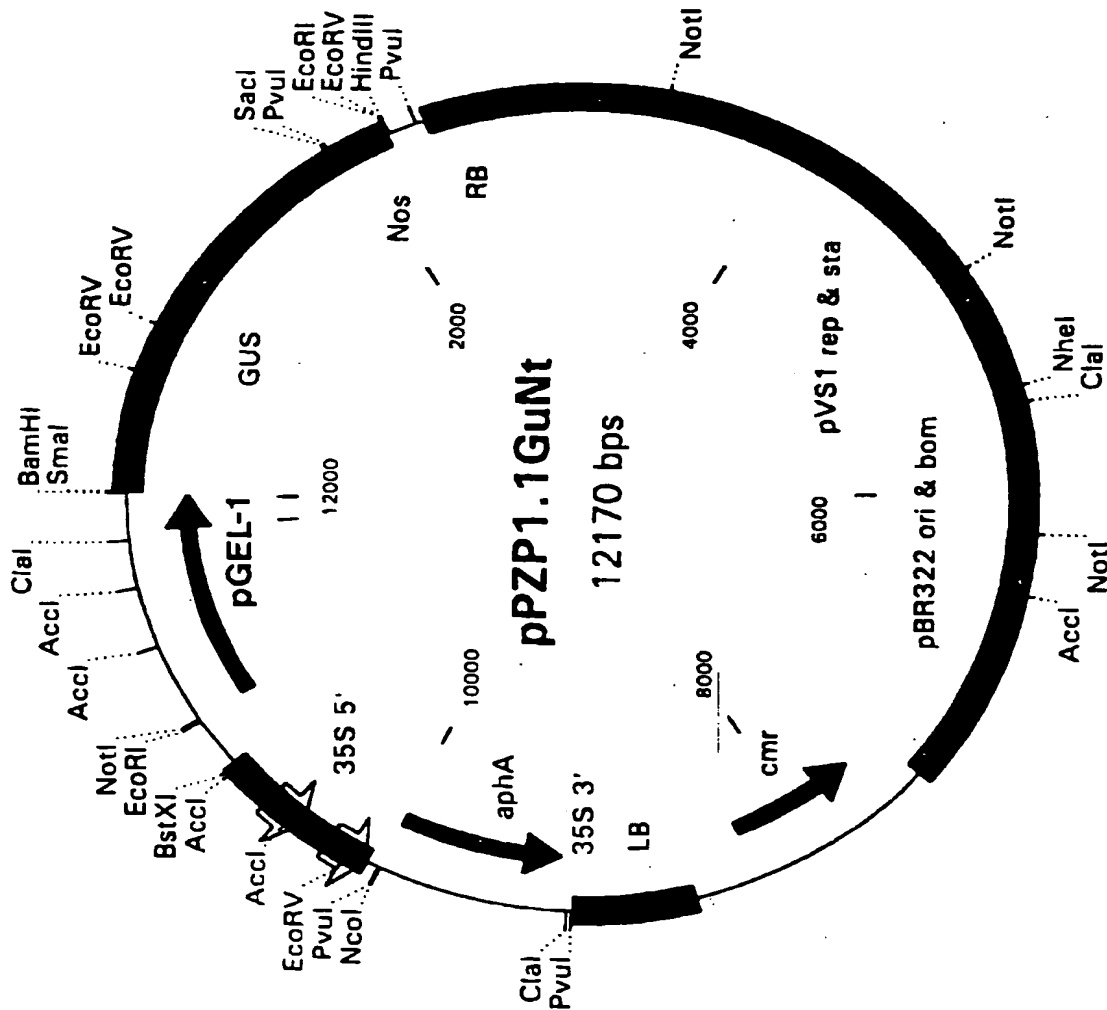


FIGURE 6A(xi)

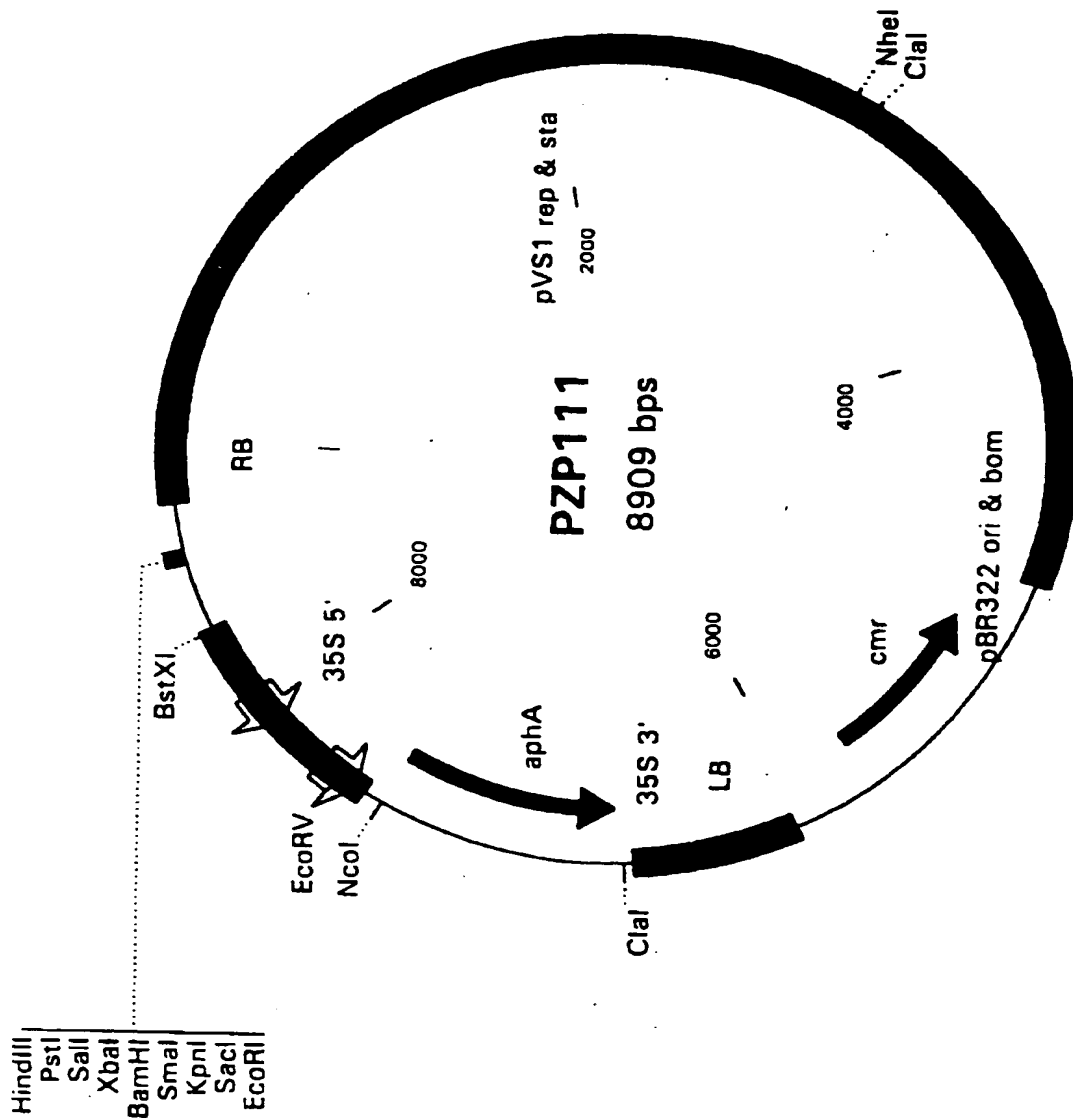
19/28

FIGURE 6A(xii)

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20/28

FIGURE 6B



Substitute Sheet
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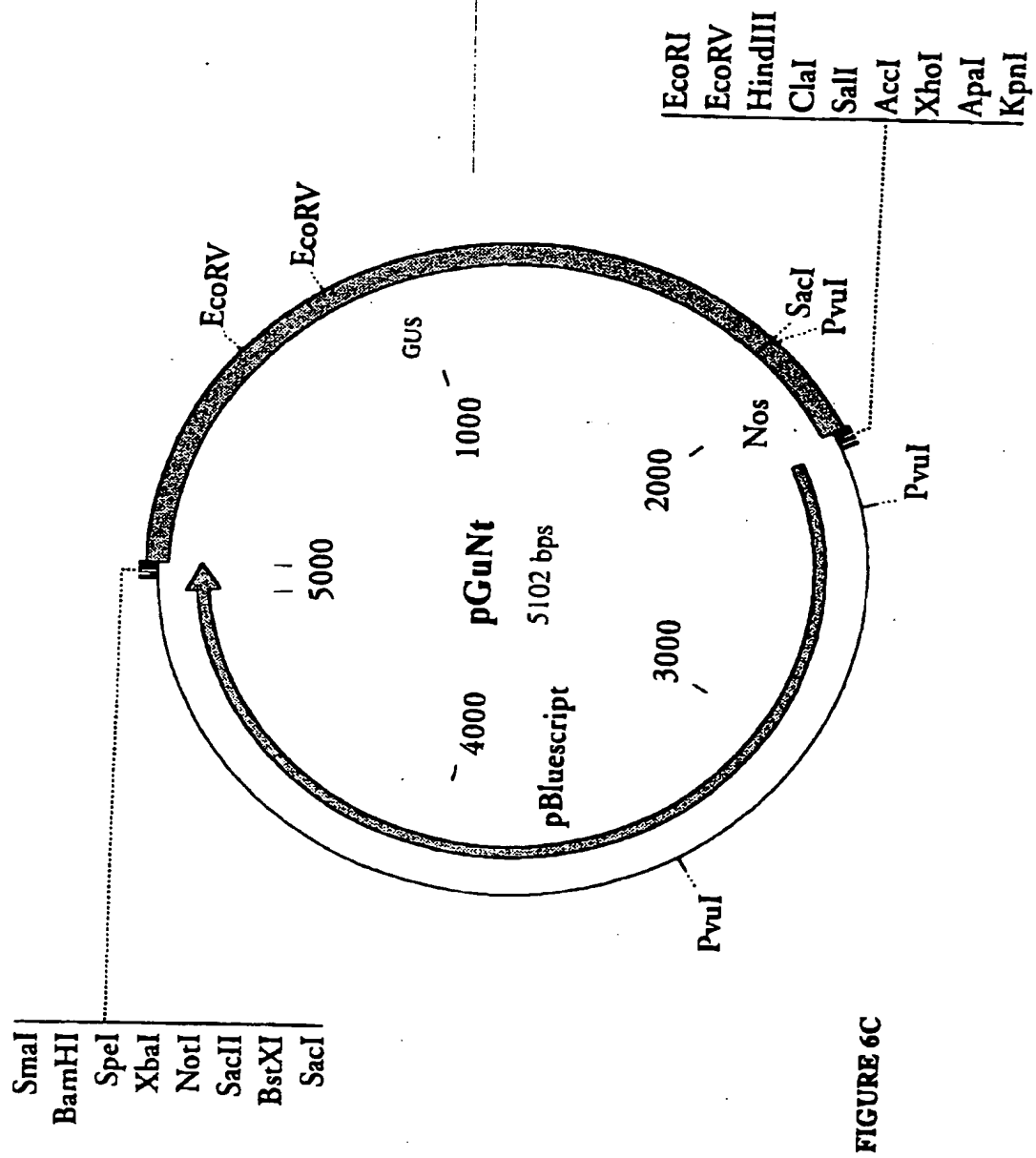


FIGURE 6C

22 / 28

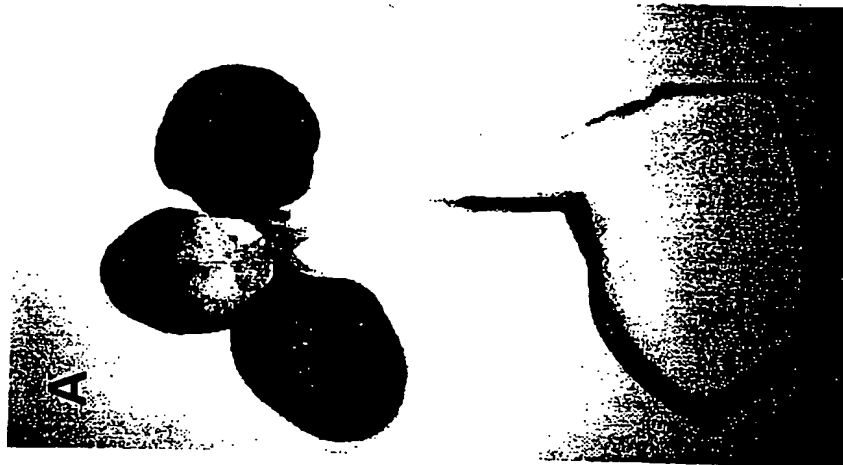
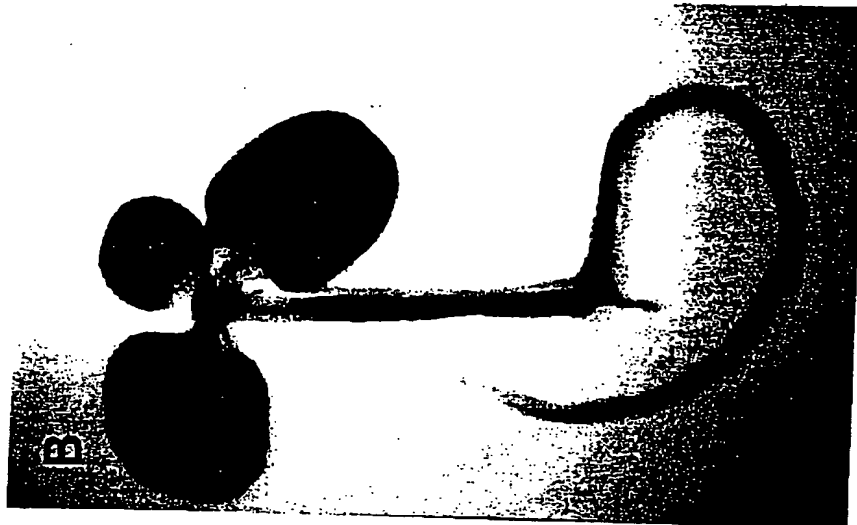
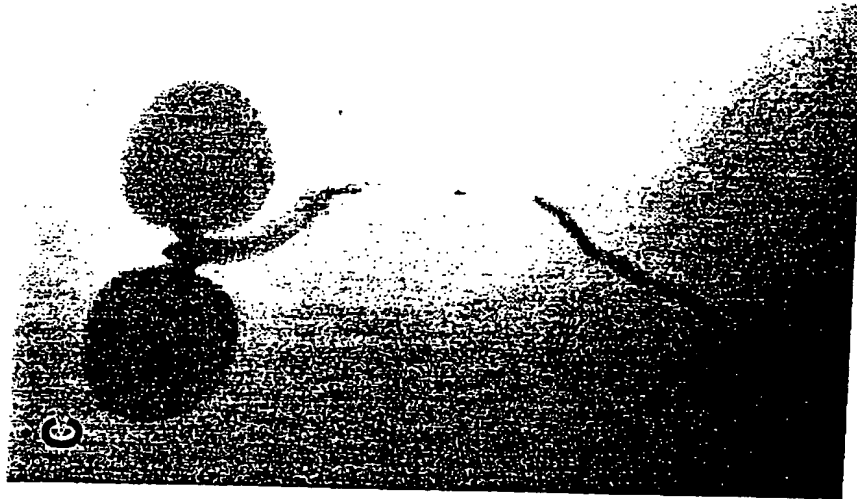


FIGURE 7

Substitute Sheet
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FIGURE 8B

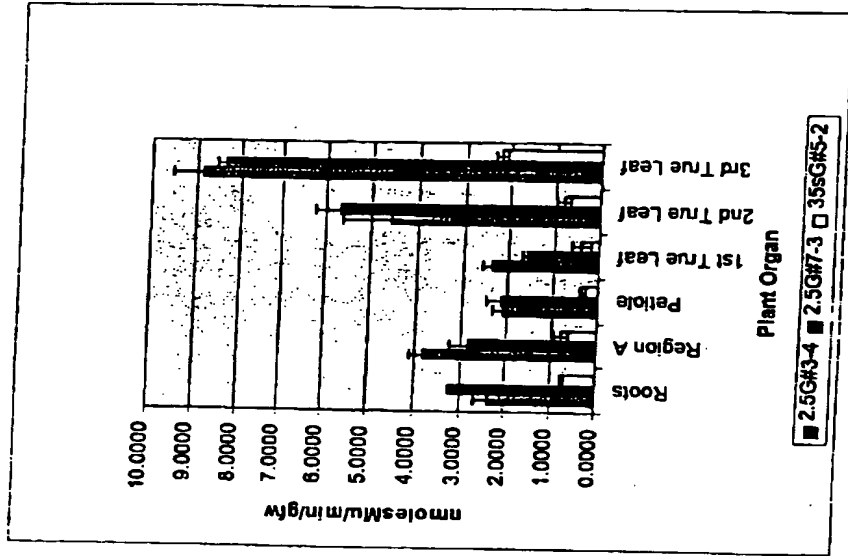
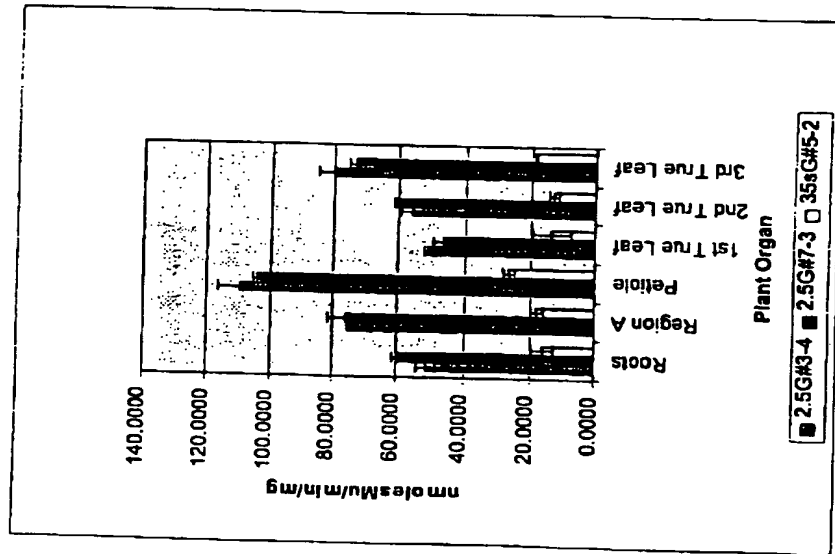


FIGURE 8A



24/28

FIGURE 9B

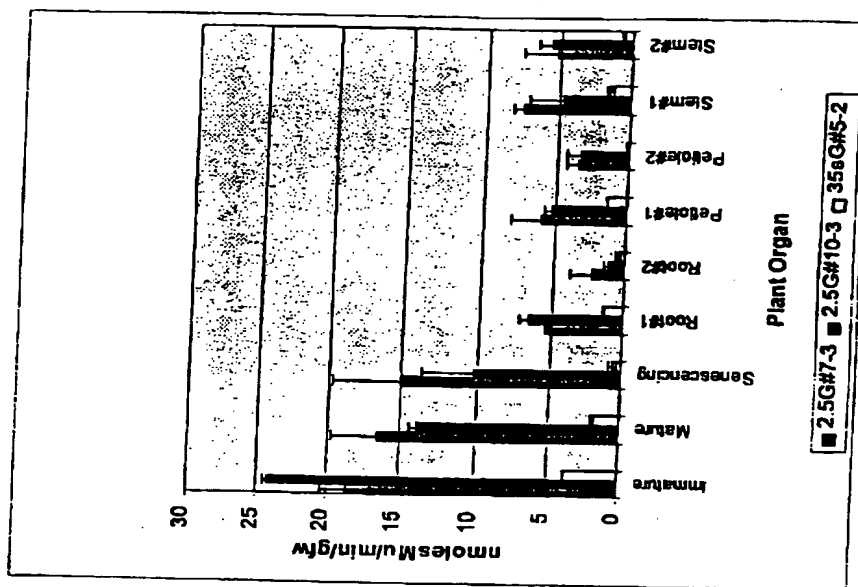
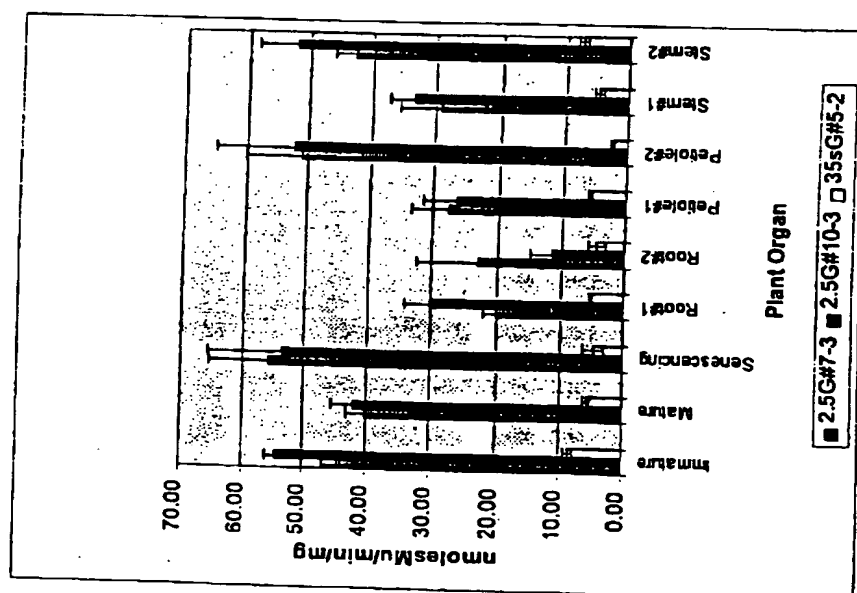


FIGURE 9A



25/28

FIGURE 10B

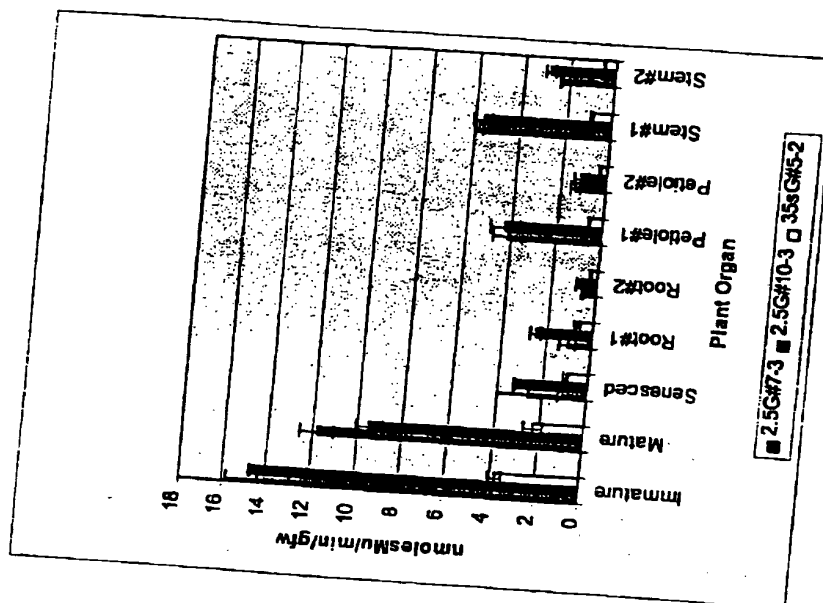
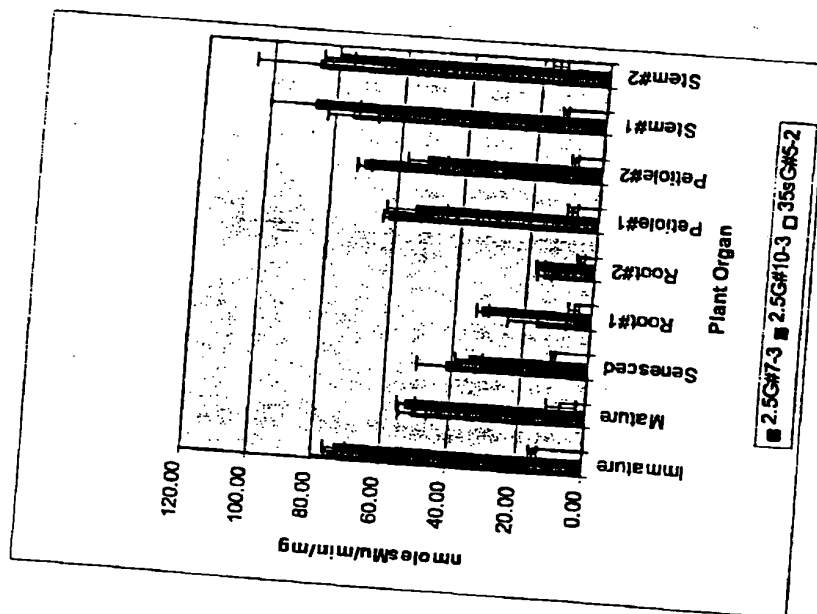


FIGURE 10A



26/28

FIGURE 11

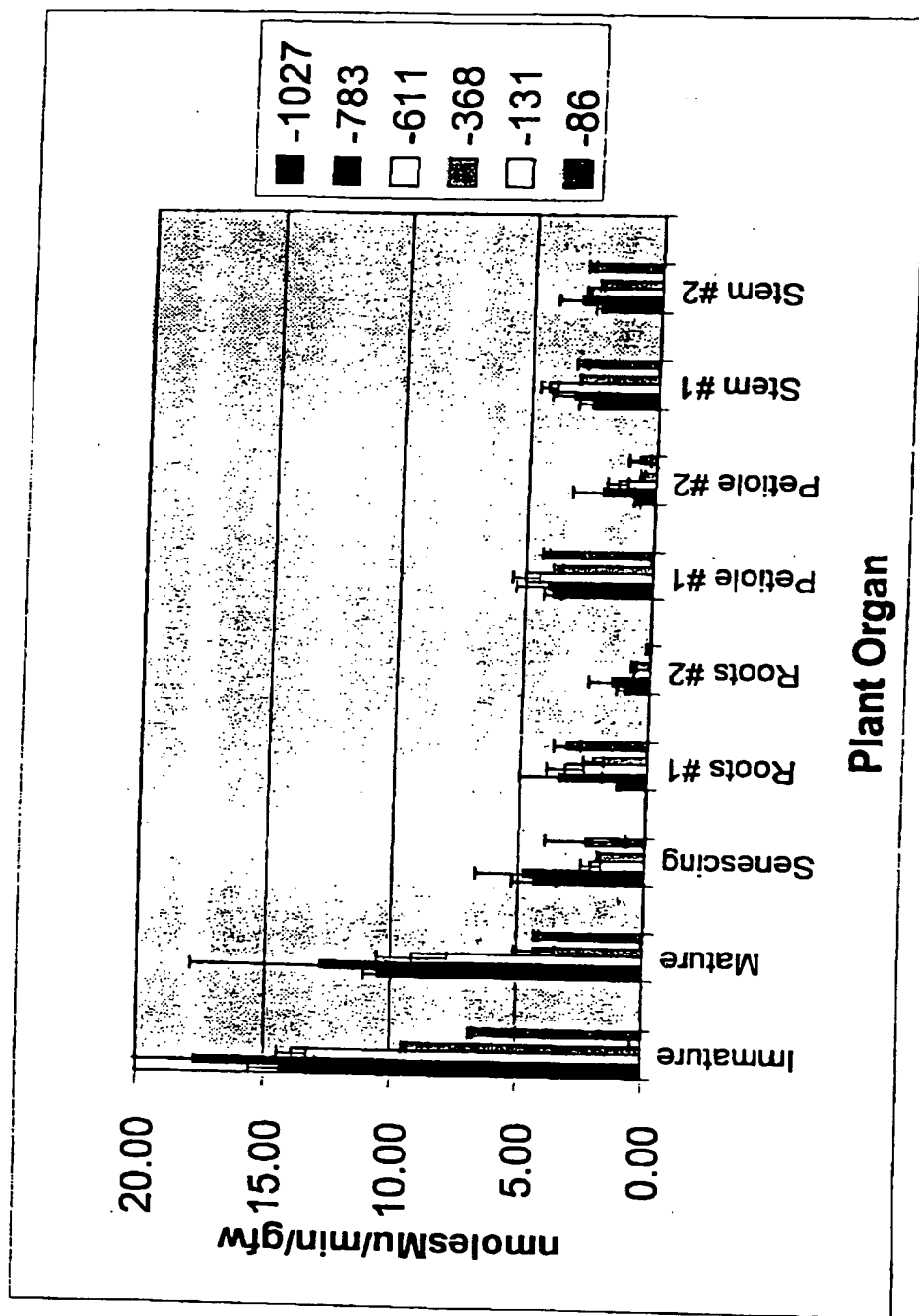
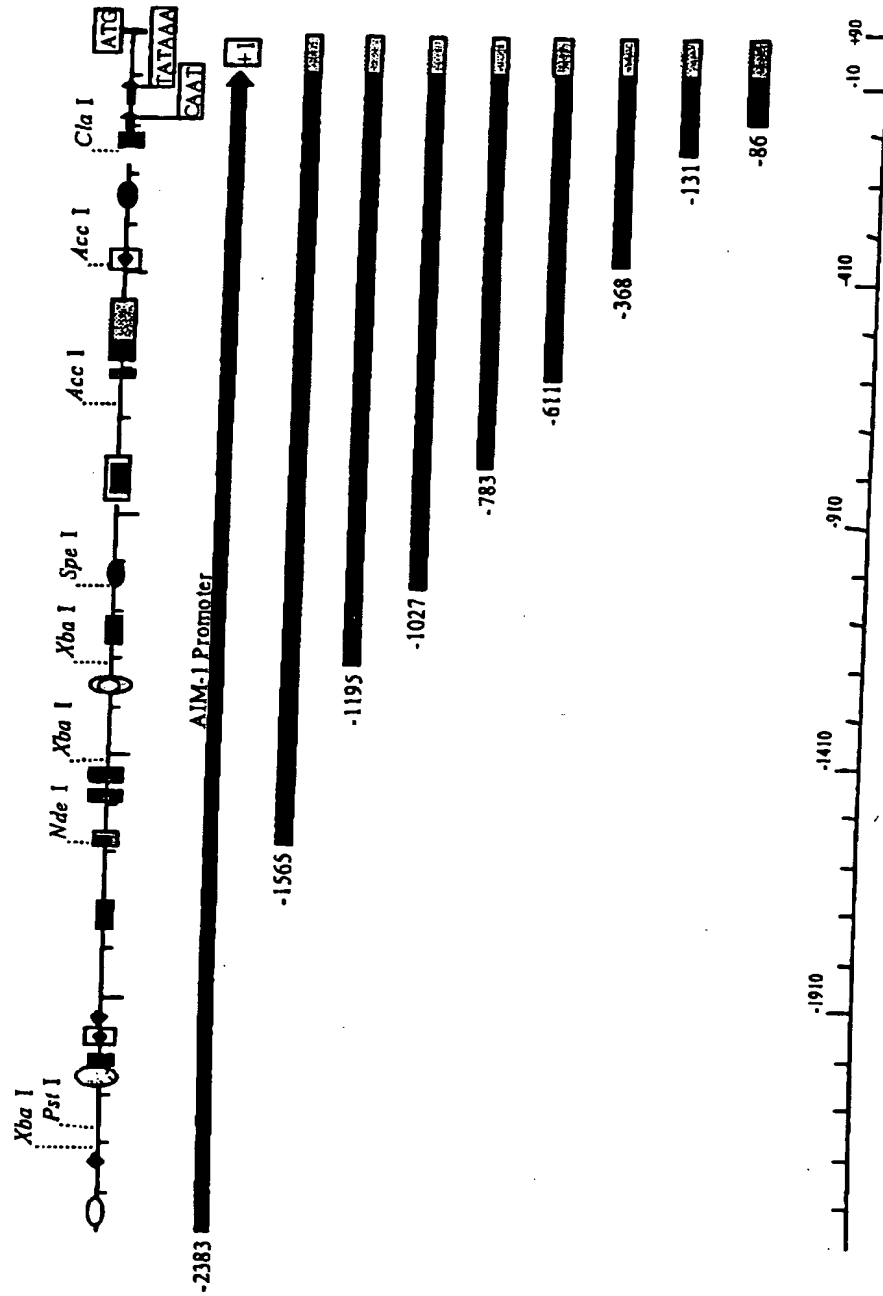
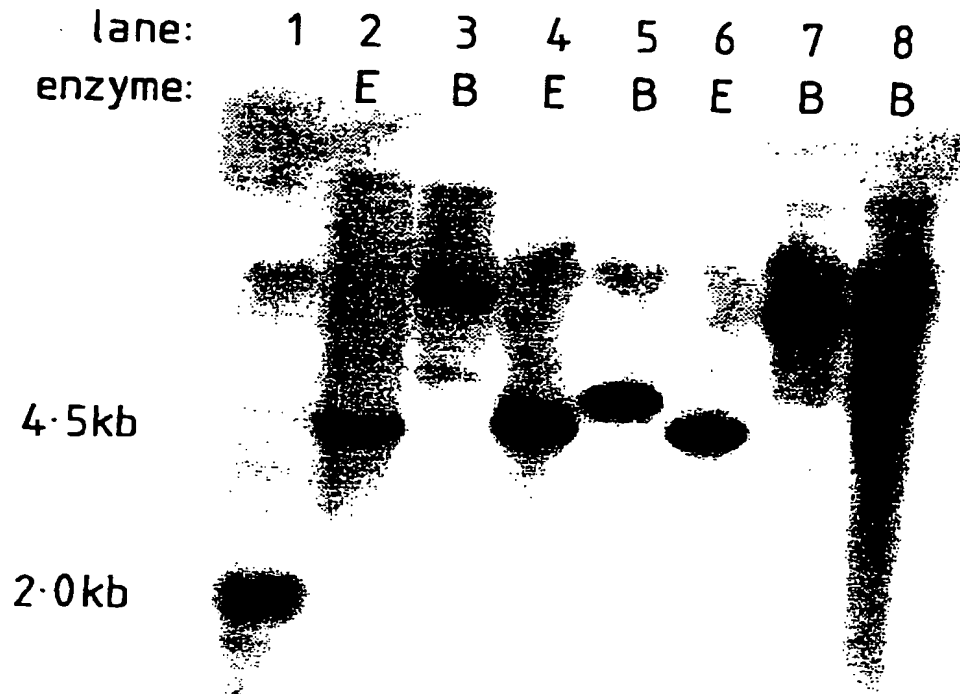


FIGURE 12



26/28

FIGURE 13